

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:28:57 ; Search time 5.63636 Seconds
(without alignments)
102.373 Million cell updates/sec

Title: US-09-743-225-1

Perfect score: 30

Sequence: 1 LKTPRV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	310	2 T34260	hypothetical prote
2	30	100.0	315	2 E87641	glucokinase family
3	30	100.0	949	2 T03030	hypothetical prote
4	30	100.0	1323	1 RRGSM	RNA-directed RNA p
5	29	96.7	38	2 B82225	hypothetical prote
6	28	93.3	997	2 S73556	MG414 homolog C12-
7	28	93.3	2325	1 A23443	pyrimidine synthe
8	27	90.0	177	2 H86710	hypothetical prote
9	27	90.0	232	2 S4944	hypothetical prote
10	27	90.0	245	2 T21654	hypothetical prote
11	27	90.0	388	2 D89979	Staphopain, Cyste
12	27	90.0	392	1 S18593	chloramphenicol re
13	27	90.0	492	2 T21797	hypothetical prote
14	27	90.0	613	2 A85079	elongation factor
15	27	90.0	620	2 F97946	hypothetical prote
16	27	90.0	633	2 T27499	hypothetical prote
17	27	90.0	1038	2 T02634	rep protein homolo
18	27	90.0	1192	2 T33157	hypothetical prote
19	26	86.7	72	2 F86064	hypothetical prote
20	26	86.7	83	2 S05975	tetracenomycin C-p
21	26	86.7	145	2 T19489	hypothetical prote
22	26	86.7	154	2 A48425	heat shock protein
23	26	86.7	158	2 C87354	hypothetical prote
24	26	86.7	214	1 D75051	probable phosphos
25	26	86.7	220	2 S75751	hypothetical prote
26	26	86.7	224	2 T32097	hypothetical prote
27	26	86.7	228	2 C75492	hypothetical prote
28	26	86.7	231	2 S73286	phycobilisome rod-
29	26	86.7	234	2 T11967	phycobilisome rod-

30 26 86.7 243 2 S25308 probable phycocyan
31 26 86.7 253 2 A71525 probable dihydrodi
32 26 86.7 255 2 T02549 hypothetical prote
33 26 86.7 257 2 G86767 N-acetylglucosamin
34 26 86.7 276 2 E72623 probable autoantig
35 26 86.7 283 2 T33705 hypothetical prote
36 26 86.7 287 2 S76288 hypothetical prote
37 26 86.7 288 2 T51059 transcription regu
38 26 86.7 306 2 H86740 protein C38C3.4.[1
39 26 86.7 307 2 H88950 hypothetical prote
40 26 86.7 327 2 T19529 hypothetical prote
41 26 86.7 331 1 DECHLM L-lactate dehydrog
42 26 86.7 332 1 DEMSLM L-lactate dehydrog
43 26 86.7 332 2 A23083 L-lactate dehydrog
44 26 86.7 332 2 S12151 L-lactate dehydrog
45 26 86.7 334 2 A47180 L-lactate dehydrog

ALIGNMENTS

RESULT 1

T34260
Hypothetical protein F38E1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000
C:Accession: T34260
R:Gattung, S.; Le T.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid F38E1.
A:Reference number: Z21495
A:Accession: T34260
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-310 <GAT>
A:Cross-references: EMBL:U41996; PIDN:AAA83477.1; CESP:F38E1.3
A:Gene: CESP:F38E1.3
C:Genetics:
A:Introns: 14/3; 69/3; 120/3; 166/3; 255/3; 294/3
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 100.0%; Score 30; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6
DB 185 LKTPRV 190

RESULT 2

E87641
glucokinase family protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: E87641
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, N.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87641
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <STO>
A:Cross-references: GB:AE005673; NID:g13424837; PIDN:AAK25129.1; GSPDB:GN00148
C:Genetics:
C:Superfamily: glucokinase

Query Match 100.0%; Score 30; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 33;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6
|||||
DB 81 LKTPRV 86

RESULT 3

T03030
hypothetical protein KIAA0365 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C:Accession: T03030
R:Lamerdin, J.E.; McCreedy, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, C.; Andreise, T.; Trankhel
Arellano, A.; Montgomery, M.; Ow, D.; Nolan, M.; Trong, S.; Kobayashi, A.; Olsen, A.O.;
submitted to the EMBL Data Library, March 1998
A:Description: Sequence analysis of an ~1 Mb region containing the MER2B gene in 19p12.
A:Reference number: Z14651
A:Accession: T03030
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-949 <LAW>
A:Cross-references: EMBL:AC004447; NID:g2978446; PIDN:AA06129.1; PID:g2978447
A:Experimental source: brain
C:Genetics:
A:Map position: 19
A:Introns: 434/1; 474/2; 637/1; 674/2; 834/1; 854/3

Query Match 100.0%; Score 30; DB 2; Length 949;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6
|||||
DB 250 LKTPRV 255

RESULT 4

RWGSN
N:Alternate names: RNA nucleotidyltransferase (EC 2.7.7.48) - strawberry mild yellow edge-associated virus
C:Species: strawberry mild yellow edge-associated virus
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 19-Jan-2001
C:Accession: JQ1426
R:Jelkmann, W.; Maiss, E.; Martin, R.R.
J. Gen. Virol. 73, 475-479, 1992
A:Title: The nucleotide sequence and genome organization of strawberry mild yellow edge-
A:Reference number: JQ1426; MUID:92166762; PMID:1339469
A:Molecule type: genomic RNA
A:Residues: 1-1323 <JEL>
A:Cross-references: GB:D12517; DDBJ:D01227; NID:g222631; PIDN:BA02082.1; PID:g222632
C:Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
C:Keywords: ATP; nucleotide binding; nucleotidyltransferase; P-loop; RNA biosynthesis; R
F:605-612/Region: nucleotide-binding motif A (P-loop)
F:668-673/Region: nucleotide-binding motif B
F:611/Binding site: ATP (Lys) #status predicted

Query Match 100.0%; Score 30; DB 1; Length 1323;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6
|||||
DB 275 LKTPRV 280

RESULT 5

B82225
hypothetical protein VC1218 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: B82225
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
L., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: B82225
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-38 <HEI>
A:Cross-references: GB:AE004202; GB:AE003852; NID:g9655698; PIDN:AAF94377.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1218
A:Map position: 1

Query Match 96.7%; Score 29; DB 2; Length 38;
Best Local Similarity 83.3%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6
|||||
DB 14 LKTPRV 19

RESULT 6

S73556
MG414 homolog C12_orf997 - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C>Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C:Accession: S73556
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkil, E.; Li, B.C.; Hermann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonia
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73556
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-997 <HIM>
A:Cross-references: EMBL:AE000023; GB:U00089; NID:g1673893; PIDN:AAB95878.1; PID:g167
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: hypothetical protein MG413

Query Match 93.3%; Score 28; DB 2; Length 997;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6
|||||
DB 308 LKTPRV 313

RESULT 7

A23443
pyrimidine synthesis multifunctional protein CAD - golden hamster
N:Contains: aspartate carbamoyltransferase (EC 2.1.3.2); carbamoyl-phosphate synthase
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 29-Aug-1987 #sequence_revision 02-Jun-1994 #text_change 18-Jun-1999
C:Accession: A38653; PS0159; A23443; A30794; A34803; I48154
R:Bein, K.; Simmer, J.P.; Evans, D.R.
J. Biol. Chem. 266, 3791-3799, 1991
A:Title: Molecular cloning of a cDNA encoding the amino end of the mammalian multifun
A:Reference number: A38653; MUID:91139675; PMID:1671675
A:Accession: A38653
A:Molecule type: mRNA
A:Residues: 1-169 <BEI>
A:Cross-references: GB:M60078; NID:gl91338; PIDN:AAA63617.1; PID:gl91339
R:Simmer, J.P.; Kelly, R.E.; Rinker Jr., A.G.; Scully, J.L.; Evans, D.R.
J. Biol. Chem. 265, 10395-10402, 1990

A;Title: Mammalian carbamyl phosphate synthetase (CPS). cDNA sequence and evolution of
 A;Reference number: A35432; MUID:90285162; PMID:1972379
 A;Accession: A35432
 A;Molecule type: mRNA
 A;Residues: 136-1455 <SIM>
 A;Cross-references: GB:J05503; NID:g191332; PIDN:AAA37062.1; PID:g191333
 R;Williams, N.K.; Simpson, R.J.; Moritz, R.L.; Pelde, Y.; Crofts, L.; Minasian, E.; Lead
 Gene 94, 283-288, 1990
 A;Title: Location of the dihydroorotase domain within trifuunctional hamster dihydroorota
 A;Reference number: PS0159; MUID:91078661; PMID:1979549
 A;Accession: PS0159
 A;Molecule type: mRNA
 A;Residues: 1403-2110 <WIL>
 A;Cross-references: GB:M33702; NID:g191172; PIDN:AAA37009.1; PID:g191173
 R;Shigesada, K.; Stark, G.R.; Maley, J.A.; Niswander, L.A.; Davidson, J.N.
 Mol. Cell. Biol. 5, 1735-1742, 1985
 A;Title: Construction of a cDNA to the hamster CAD gene and its application toward defin
 A;Reference number: A23443; MUID:85267690; PMID:2862577
 A;Accession: A23443
 A;Molecule type: mRNA
 A;Residues: 2074-2225 <SHI>
 A;Cross-references: GB:M1242; NID:g191330; PIDN:AAA37061.1; PID:g387067
 R;Maley, J.A.; Davidson, J.N.
 Biochem. Biophys. Res. Commun. 154, 1047-1053, 1988
 A;Title: Identification of the junction between the glutamine amidotransferase and carba
 A;Reference number: A30794; MUID:88309082; PMID:2900634
 A;Accession: A30794
 A;Molecule type: mRNA
 A;Residues: 246-464 <MAL>
 A;Cross-references: GB:M21927
 R;Simmer, J.P.; Kelly, R.E.; Rinker Jr., A.G.; Zimmermann, B.H.; Scully, J.L.; Kim, H.;
 Proc. Natl. Acad. Sci. U.S.A. 87, 174-178, 1990
 A;Title: Mammalian dihydroorotase: nucleotide sequence, peptide sequences, and evolution
 A;Reference number: A34803; MUID:90115834; PMID:1967494
 A;Accession: A34803
 A;Molecule type: mRNA
 A;Residues: 1391-1870 <SI2>
 A;Cross-references: GB:M28866; NID:g191363; PIDN:AAA37073.1; PID:g191364
 A;Note: parts of this sequence were confirmed by peptide sequencing
 R;Farnham, P.J.; Kollmar, R.
 Cell Growth Differ. 1, 179-189, 1990
 A;Title: Characterization of the 5' end of the growth-regulated Syrian hamster CAD gene.
 A;Reference number: I48154; MUID:91190717; PMID:1982061
 A;Accession: I48154
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-73 <RES>
 A;Cross-references: GB:M31621; NID:g191326; PIDN:AAA37060.1; PID:g553847
 C;Genetics:
 A;Gene: CAD
 A;Map position: B9 short arm
 A;Introns: 28/1
 C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Ba
 carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phos
 C;Keywords: hydrolase; ligase; methyltransferase; multifunctional enzyme; phosphoprotein
 F:4-1442/Domain: carbamoyl-phosphate synthase (ammonia) homology <CPA>
 F:4-354/Domain: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homolog
 F:178-354/Domain: trpG homology <TRG>
 F:395-1439/Domain: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homc
 F:395-845/Domain: biotin carboxylase homology <BC1>
 F:934-1380/Domain: biotin carboxylase homology <BC2>
 F:1457-1801/Domain: Bacillus dihydroorotase homology <DHO>
 F:1924-2222/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
 F:253/Active site: Cys #status predicted

Query Match 93.3%; Score 28; DB 1; Length 2225;
 Best Local Similarity 83.3%; Pred. No. 6.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKTPRV 6
 :|||||
 Db 164 IKTPRV 169

RESULT 8

H86710
 hypothetical protein ygiJ [imported] - Lactococcus lactis subsp. lactis (strain IL140
 C;Species: Lactococcus lactis subsp. lactis
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C;Accession: H86710
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissbach, J.; Eh
 Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
 A;Reference number: A86625; MUID:21235186; PMID:11337471
 A;Accession: H86710
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-177 <STO>
 A;Cross-references: GB:AE005176; PID:g12723597; PIDN:AAK04786.1; GSPDB:GN00146
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: ygiJ

Query Match 90.0%; Score 27; DB 2; Length 177;
 Best Local Similarity 83.3%; Pred. No. 91;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKTPRV 6
 :|||||
 Db 84 LKTPRL 89

RESULT 9

S24944
 hypothetical protein 7 - Rhizobium meliloti plasmid pRmeGR4b
 C;Species: Rhizobium meliloti
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Apr-2000
 C;Accession: S35087; S24944
 R;Soto, M.J.; Zorzano, A.; Mercado-Bianco, J.; Lepek, V.; Olivares, J.; Toro, N.
 J. Mol. Biol. 229, 570-576, 1993
 A;Title: Nucleotide sequence and characterization of Rhizobium meliloti nodulation co
 A;Reference number: S35086; MUID:93156068; PMID:8429568
 A;Accession: S35087
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-232 <SO2>
 A;Cross-references: EMBL:X66124; NID:g46324; PIDN:CAA46913.1; PID:g46326
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1992
 C;Genetics:
 A;Genome: plasmid
 C;Superfamily: Rhizobium meliloti plasmid pRmeGR4b hypothetical protein 7

Query Match 90.0%; Score 27; DB 2; Length 232;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKTPRV 6
 :|||||
 Db 70 LRTPRV 75

RESULT 10

T21654
 hypothetical protein F32D8.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C;Accession: T21654
 R;Wilkinson, J.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: Z19454
 A;Accession: T21654
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-245 <WIL>
 A;Cross-references: EMBL:Z74031; PIDN:CAA98455.1; GSPDB:GN00023; CESP:F32D8.3
 A;Experimental source: clone F32D8

Query Match 93.3%; Score 28; DB 1; Length 2225;
 Best Local Similarity 83.3%; Pred. No. 6.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKTPRV 6
 :|||||
 Db 164 IKTPRV 169

C:Genetics:

A:Gene: CESP:F32D8.3

A:Map position: 5

A:Introns: 61/1: 83/3

C:Superfamily: Caenorhabditis elegans hypothetical protein F32D8.3

Query Match 90.0%; Score 27; DB 2; Length 245;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6

|||||

Db 32 LKTPKV 37

RESULT 11

D89979

Staphopain, Cysteine Proteinase [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: D89979

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uli, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: D89979

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-388 <KUR>

A:Cross-references: GB:BA000018; PID:gl13701702; PIDN:BA842995.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SAI725

Query Match 90.0%; Score 27; DB 2; Length 388;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6

|||||

Db 170 LKTPRL 175

RESULT 12

S18593

Chloramphenicol resistance protein - Streptomyces lividans

C:Species: Streptomyces lividans

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S18593

R:Dirlich, W.; Betzler, M.; Schrempf, H.

Mol. Microbiol. 5, 2789-2797, 1991

A:Title: An amplifiable and deletable chloramphenicol-resistance determinant of *Streptomyces lividans*

A:Reference number: S18593; MUID:92140043; PMID:1779766

A:Accession: S18593

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 <DIT>

A:Cross-references: EMBL:X59868; NID:g47159; PIDN:CAA42594.1; PID:g47160

C:Superfamily: Streptomyces lividans chloramphenicol resistance protein

C:Keywords: antibiotic resistance; transmembrane protein

Query Match 90.0%; Score 27; DB 1; Length 392;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6

|||||

Db 200 LKTPRL 205

RESULT 13

F97946

hypothetical protein typA [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae

T21797

hypothetical protein T05G11.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T21797; T24551

R:Gardner, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19472

A:Accession: T21797

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-492 <WIL>

A:Cross-references: EMBL:Z81529; PIDN:CAB04303.1; GSPDB:GN00023; CESP:T05G11.1

A:Experimental source: clone F35E8

R:Wall, M.

submitted to the EMBL Data Library, June 1998

A:Reference number: Z19906

A:Accession: T24551

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-492 <WIL>

A:Cross-references: EMBL:AL023816; PIDN:CAA19434.1; GSPDB:GN00023; CESP:T05G11.1

A:Experimental source: clone T05G11

C:Genetics:

A:Gene: CESP:T05G11.1

A:Map position: 5

A:Introns: 10/1; 177/1; 222/3

Query Match

90.0%; Score 27; DB 2; Length 492;

Best Local Similarity 83.3%; Pred. No. 2.5e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6

|||||

Db 438 LKTPRM 443

RESULT 14

A95079

elongation factor Tu family protein [imported] - Streptococcus pneumoniae (strain TIG

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001

C:Accession: A95079

R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappel

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris

A:Title: Complete genome sequence of a virulent isolate of *Streptococcus pneumoniae*.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: A95079

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-613 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK74826.1; PID:gl4972156; GSPDB:GN00164; TIGR:

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP0681

C:Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu ho

Query Match

90.0%; Score 27; DB 2; Length 613;

Best Local Similarity 66.7%; Pred. No. 3.1e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6

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Db 562 LKTPRI 567

RESULT 15

F97946

hypothetical protein typA [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C/Accession: F97946
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: F97946
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-620 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99402.1; PID:g15458179; GSPDB:GN00174
C:Genetics:
A:Gene: ttpA
C:Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu homol

Query Match 90.0%; Score 27; DB 2; Length 620;
Best Local Similarity 66.7%; Pred. NO. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTPRV 6
:||||:
Db 569 IKTPRI 574

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Job time : 7.63636 secs